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RAW SEQUENCE LISTING

DATE: 08/22/2002 P.6

PATENT APPLICATION: US/10/084,507B

TIME: 16:37:46

Input Set : A:\10807423.app

Output Set: N:\CRF4\08222002\J084507B.raw

3 <110> APPLICANT: MUNROE, DONALD G.
 4 KAMBOJ, RAJENDER
 5 PETERS, DIANA
 6 KOOSHESH, FATEMEH
 7 VYAS, TEJAL B.
 8 GUPTA, ASHWANI K.
 10 <120> TITLE OF INVENTION: AN ISOLATED HUMAN EDG-4 RECEPTOR
 12 <130> FILE REFERENCE: 108074-00023
 14 <140> CURRENT APPLICATION NUMBER: 10/084,507B
 C--> 15 <141> CURRENT FILING DATE: 2002-08-12
 17 <150> PRIOR APPLICATION NUMBER: 09/222,995
 18 <151> PRIOR FILING DATE: 1998-12-30
 20 <150> PRIOR APPLICATION NUMBER: 60/109,885
 21 <151> PRIOR FILING DATE: 1998-11-25
 23 <150> PRIOR APPLICATION NUMBER: 60/080,610
 24 <151> PRIOR FILING DATE: 1998-04-03
 26 <150> PRIOR APPLICATION NUMBER: 60/070,185
 27 <151> PRIOR FILING DATE: 1997-12-30
 29 <160> NUMBER OF SEQ ID NOS: 24
 31 <170> SOFTWARE: PatentIn Ver. 2.1
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 35
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Rattus sp.
 38 <400> SEQUENCE: 1
 39 gagaagggttc aggaacacta caattacacc aagga 35
 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 25
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Artificial Sequence
 47 <220> FEATURE:
 48 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 49 primer
 51 <400> SEQUENCE: 2
 52 attataccaa ggagacgctg gaaac 25
 55 <210> SEQ ID NO: 3
 56 <211> LENGTH: 25
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 62 primer
 64 <400> SEQUENCE: 3

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65 agagagcaag gtattggcta cgaag                25
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69 <211> LENGTH: 22
70 <212> TYPE: DNA
71 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
75     primer
77 <400> SEQUENCE: 4
78 tcctctcctc gtcacatttc cc                    22
81 <210> SEQ ID NO: 5
82 <211> LENGTH: 26
83 <212> TYPE: DNA
84 <213> ORGANISM: Artificial Sequence
86 <220> FEATURE:
87 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
88     primer
90 <400> SEQUENCE: 5
91 gcattcaciaa gaaattactc tgaggc                26
94 <210> SEQ ID NO: 6
95 <211> LENGTH: 26
96 <212> TYPE: DNA
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
101     primer
103 <400> SEQUENCE: 6
104 gagccccacc atgggcagct tgtact                26
107 <210> SEQ ID NO: 7
108 <211> LENGTH: 26
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
114     primer
116 <400> SEQUENCE: 7
117 gcattcaciaa gaaattactc tgaggc                26
120 <210> SEQ ID NO: 8
121 <211> LENGTH: 34
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
127     primer
129 <400> SEQUENCE: 8
130 tttaaaaaagc ttcccacat gggcagcttg tact        34
133 <210> SEQ ID NO: 9
134 <211> LENGTH: 37
135 <212> TYPE: DNA

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138 <220> FEATURE:
139 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
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146 <210> SEQ ID NO: 10
147 <211> LENGTH: 32
148 <212> TYPE: DNA
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
153     primer
155 <400> SEQUENCE: 10
156 tatatatcta gaggaatgt gacgaggaga gg 32
159 <210> SEQ ID NO: 11
160 <211> LENGTH: 33
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
166     primer
168 <400> SEQUENCE: 11
169 ttttaaaggta ccgccaccat gggcagcttg tac 33
172 <210> SEQ ID NO: 12
173 <211> LENGTH: 33
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
179     primer
181 <400> SEQUENCE: 12
182 tatatatcta gagaccaccg tggtgccctc cag 33
185 <210> SEQ ID NO: 13
186 <211> LENGTH: 445
187 <212> TYPE: DNA
188 <213> ORGANISM: Homo sapiens
190 <400> SEQUENCE: 13
191 aaagcccccatt ggccccagca ggcctctgag cccaccatg ggcagcttgt actcggagta 60
192 cctgaacccc aacaagggtcc aggaacacta taattatacc aaggagacgc tggaaacgca 120
193 ggagacgacc tcccgcagg tggcctcggc attcatcgtc atcctctgtt gcgccattgt 180
194 ggtggaaaac cttctggtgc tcattgcggt ggcccgaac agcaagttcc actcggcaat 240
195 gtacctgttt ctgggcaacc tggccgcctc cgatctactg gcaggcgtgg ccttcgtagc 300
196 caataccttg ctctctggct ctgtcacgct gaggctgacg cctgtgcagt ggtttgcccg 360
197 ggacggtctg ccttcacac gctctcggcc tctgtcttca gcctcctggc catcgccatt 420
198 gagcgccacg tggccattgc aaagg 445
201 <210> SEQ ID NO: 14
202 <211> LENGTH: 364
203 <212> TYPE: DNA

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207 aaagcccat ggcccagca ggcctctgag cccaccatg ggcagcttgt actcggagta 60
208 cctgaacccc aacaaggtcc aggaacacta taattatacc aaggagacgc tggaaacgca 120
209 ggagacgacc tcccgcagg tggcctcggc cttcatcgtc atcctctgtt gcgccattgt 180
210 ggtggaaaac cttctggtgc tcattgcggt ggcccgaac agcaagttcc actcggcaat 240
211 gtacctgttt ctgggcaacc tggccgcctc cgatctactg gcaggcgtgg ccttcgtagc 300
212 caataccttg ctctctggct ctgtcacgct gaggctgacg cctgtgcagt ggtttgcccg 360
213 ggac 364
216 <210> SEQ ID NO: 15
217 <211> LENGTH: 369
218 <212> TYPE: DNA
219 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 15
222 agttctgaaa gcccctatggc cccagcaggc ctctgagccc caccatgggc agcttggtact 60
223 cggagtacct gaacccaac aaggtccagg aacactataa ttataccaag gagacgctgg 120
224 aaacgcagga gacgacctcc cgccaggtgg gctcggcctt catcgtcatc ctctgttgcg 180
225 ccattgtggt ggaaaacctt ctggtgctca ttgcggtggc ccgaaacagc aagttccact 240
226 cggcaatgta cctgtttctg ggcaacctgg ccgcctccga tctactggca ggcgtggctt 300
227 cgtagccaat accttgctct ctggctctgt cacgctgagg ctgacgcctg tgcagtgggt 360
228 tgcccggga 369
231 <210> SEQ ID NO: 16
232 <211> LENGTH: 1170
233 <212> TYPE: DNA
234 <213> ORGANISM: Homo sapiens
236 <220> FEATURE:
237 <221> NAME/KEY: CDS
238 <222> LOCATION: (38)..(1096)
240 <220> FEATURE:
241 <221> NAME/KEY: MOD_RES
242 <222> LOCATION: (273)
243 <223> OTHER INFORMATION: Leu or Phe
245 <400> SEQUENCE: 16
246 aaagcccat ggcccagca ggcctctgag cccacc atg ggc agc ttg tac tcg 55
247 Met Gly Ser Leu Tyr Ser
248 1 5
250 gag tac ctg aac ccc aac aag gtc cag gaa cac tat aat tat acc aag 103
251 Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu His Tyr Asn Tyr Thr Lys
252 10 15 20
254 gag acg ctg gaa acg cag gag acg acc tcc cgc cag gtg gcc tcg gcc 151
255 Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser Arg Gln Val Ala Ser Ala
256 25 30 35
258 ttc atc gtc atc ctc tgt tgc gcc att gtg gtg gaa aac ctt ctg gtg 199
259 Phe Ile Val Ile Leu Cys Cys Ala Ile Val Val Glu Asn Leu Leu Val
260 40 45 50
262 ctc att gcg gtg gcc cga aac agc aag ttc cac tcg gca atg tac ctg 247
263 Leu Ile Ala Val Ala Arg Asn Ser Lys Phe His Ser Ala Met Tyr Leu
264 55 60 65 70
266 ttt ctg ggc aac ctg gcc gcc tcc gat cta ctg gca ggc gtg gcc ttc 295

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267	Phe	Leu	Gly	Asn	Leu	Ala	Ala	Ser	Asp	Leu	Leu	Ala	Gly	Val	Ala	Phe	
268					75					80				85			
270	gta	gcc	aat	acc	ttg	ctc	tct	ggc	tct	gtc	acg	ctg	agg	ctg	acg	cct	343
271	Val	Ala	Asn	Thr	Leu	Leu	Ser	Gly	Ser	Val	Thr	Leu	Arg	Leu	Thr	Pro	
272				90					95					100			
274	gtg	cag	tgg	ttt	gcc	cgg	gag	ggc	tct	gcc	ttc	atc	acg	ctc	tcg	gcc	391
275	Val	Gln	Trp	Phe	Ala	Arg	Glu	Gly	Ser	Ala	Phe	Ile	Thr	Leu	Ser	Ala	
276			105					110					115				
278	tct	gtc	ttc	agc	ctc	ctg	gcc	atc	gcc	att	gag	cgc	cac	gtg	gcc	att	439
279	Ser	Val	Phe	Ser	Leu	Leu	Ala	Ile	Ala	Ile	Glu	Arg	His	Val	Ala	Ile	
280		120					125					130					
282	gcc	aag	gtc	aag	ctg	tat	ggc	agc	gac	aag	agc	tgc	cgc	atg	ctt	ctg	487
283	Ala	Lys	Val	Lys	Leu	Tyr	Gly	Ser	Asp	Lys	Ser	Cys	Arg	Met	Leu	Leu	
284	135					140					145				150		
286	ctc	atc	ggg	gcc	tcg	tgg	ctc	atc	tcg	ctg	gtc	ctc	ggg	ggc	ctg	ccc	535
287	Leu	Ile	Gly	Ala	Ser	Trp	Leu	Ile	Ser	Leu	Val	Leu	Gly	Gly	Leu	Pro	
288				155					160					165			
290	atc	ctt	ggc	tgg	aac	tgc	ctg	ggc	cac	ctc	gag	gcc	tgc	tcc	act	gtc	583
291	Ile	Leu	Gly	Trp	Asn	Cys	Leu	Gly	His	Leu	Glu	Ala	Cys	Ser	Thr	Val	
292				170					175					180			
294	ctg	cct	ctc	tac	gcc	aag	cat	tat	gtg	ctg	tgc	gtg	gtg	acc	atc	ttc	631
295	Leu	Pro	Leu	Tyr	Ala	Lys	His	Tyr	Val	Leu	Cys	Val	Val	Thr	Ile	Phe	
296			185					190					195				
298	tcc	atc	atc	ctg	ttg	gcc	atc	gtg	gcc	ctg	tac	gtg	cgc	atc	tac	tgc	679
299	Ser	Ile	Ile	Leu	Leu	Ala	Ile	Val	Ala	Leu	Tyr	Val	Arg	Ile	Tyr	Cys	
300		200					205					210					
302	gtg	gtc	cgc	tca	agc	cac	gct	gac	atg	gcc	gcc	ccg	cag	acg	cta	gcc	727
303	Val	Val	Arg	Ser	Ser	His	Ala	Asp	Met	Ala	Ala	Pro	Gln	Thr	Leu	Ala	
304	215					220					225				230		
306	ctg	ctc	aag	acg	gtc	acc	atc	gtg	cta	ggc	gtc	ttt	atc	gtc	tgc	tgg	775
307	Leu	Leu	Lys	Thr	Val	Thr	Ile	Val	Leu	Gly	Val	Phe	Ile	Val	Cys	Trp	
308				235					240					245			
310	ctg	ccc	gcc	ttc	agc	atc	ctc	ctt	ctg	gac	tat	gcc	tgt	ccc	gtc	cac	823
311	Leu	Pro	Ala	Phe	Ser	Ile	Leu	Leu	Leu	Asp	Tyr	Ala	Cys	Pro	Val	His	
312				250					255					260			
314	tcc	tgc	ccg	atc	ctc	tac	aaa	gcc	cac	tac	ytt	ttc	gcc	gtc	tcc	acc	871
W--> 315	Ser	Cys	Pro	Ile	Leu	Tyr	Lys	Ala	His	Tyr	Xaa	Phe	Ala	Val	Ser	Thr	
316			265					270					275				
318	ctg	aat	tcc	ctg	ctc	aac	ccc	gtc	atc	tac	acg	tgg	cgc	agc	cgg	gac	919
319	Leu	Asn	Ser	Leu	Leu	Asn	Pro	Val	Ile	Tyr	Thr	Trp	Arg	Ser	Arg	Asp	
320		280					285					290					
322	ctg	cgg	cgg	gag	gtg	ctt	cgg	ccg	ctg	cag	tgc	tgg	cgg	ccg	ggg	gtg	967
323	Leu	Arg	Arg	Glu	Val	Leu	Arg	Pro	Leu	Gln	Cys	Trp	Arg	Pro	Gly	Val	
324	295					300				305					310		
326	ggg	gtg	caa	gga	cgg	agg	cgg	ggc	ggg	acc	ccg	ggc	cac	cac	ctc	ctg	1015
327	Gly	Val	Gln	Gly	Arg	Arg	Arg	Gly	Gly	Thr	Pro	Gly	His	His	Leu	Leu	
328				315					320					325			
330	cca	ctc	cgc	agc	tcc	agc	tcc	ctg	gag	agg	ggc	atg	cac	atg	ccc	acg	1063
331	Pro	Leu	Arg	Ser	Ser	Ser	Ser	Leu	Glu	Arg	Gly	Met	His	Met	Pro	Thr	

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/084,507B

DATE: 08/22/2002
TIME: 16:37:47

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:16; Xaa Pos. 273

Seq#:17; Xaa Pos. 273

VERIFICATION SUMMARY

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Input Set : A:\10807423.app

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:871

L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:272

L:424 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:

L:455 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE: